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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: Thu Oct 04 15:09:27 EDT 2007

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Application No: 10537075 Version No: 2.0

Input Set:

Output Set:

Started: 2007-09-20 12:06:58.250
Finished: 2007-09-20 12:06:59.574
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 324 ms
Total Warnings: 5
Total Errors: 0
No. of SeqIDs Defined: 24
Actual SeqID Count: 24

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SEQUENCE LISTING

<110> Kessler, Maria
Zelinski, Thomas
Hauer, Bernhard

<120> L-RHAMNOSE-INDUCIBLE EXPRESSION SYSTEMS

<130> 12810-00091-US

<140> 10537075

<141> 2005-06-01

<150> PCT/EP2003/013367

<151> 2003-11-27

<150> DE 102 56 381.0

<151> 2002-12-02

<160> 24

<170> PatentIn version 3.3

<210> 1

<211> 2046

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (288)..(1121)

<223> coding for rhaS (positive regulator of rhaBAD operon)

<220>

<221> misc_feature

<222> (1108)..(2043)

<223> coding for rhaR (positive regulator of rhaRS operon)

<220>

<221> protein_bind

<222> (56)..(72)

<223> potential RhaS binding site

<220>

<221> protein_bind

<222> (89)..(105)

<223> potential RhaS binding site

<220>

<221> protein_bind

<222> (172)..(203)

<223> potential RhaR binding site

<220>

<221> protein_bind

<222> (210)..(241)

<223> potential RhaR binding site

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<222> (24)
<223> potential start of transcription (complement)

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cacaatttgc tgaattgtgg tgatgtgatg ctaccgcat ttctgaaaaa ttcacgctgt 180
atcttgaaaa atcgacgttt ttacgtgggt ttccgctcga aaatttaagg taagaacctg 240
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cgggtattca tgtgtttaat gggcagccct ataccatcac cgggtggcacg gtctgtttcg 480
tacgcgatca tgatcggcat ctgtatgaac ataccgataa tctgtgtctg accaatgtgc 540
tgtatcgctc gccggatcga tttcagtttc tcgccgggct gaatcagttg ctgccacaag 600
agctggatgg gcagtatccg tctcactggc gcgttaacca cagcgtattg cagcaggtgc 660
gacagctggg tgcacagatg gaacagcagg aaggggaaaa tgatttacct tcgaccgcca 720
gtcgcgagat cttgtttatg caattactgc tcttgctgcg taaaagcagt ttgcaggaga 780
acctgaaaaa cagcgcacat cgtctcaact tgcttctggc ctggctggag gaccattttg 840
ccgatgaggt gaattgggat gccgtggcgg atcaattttc tctttcactg cgtacgctac 900
atcggcagct taagcagcaa acgggactga cgcctcagcg atacctgaac cgctgcgac 960
tgatgaaagc ccgacatctg ctacgccaca gcgagggcag cgttactgac atcgctatc 1020
gctgtggatt cagcgacagt aaccactttt cgacgctttt tcgccgagag ttttaactgg 1080
caccgctgta tattcgccag ggacgggatg gctttctgca ataacgcgaa tcttctcaac 1140
gtatttgtac gccatattgc gaataatcaa ctctgttctc tggccgaggt agccacgggt 1200
gcgcatcagt taaaacttct caaagatgat ttttttgcca gcgaccagca ggcagtcgct 1260
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cgtggcgatc tcttttacat tcatgtgac gataaacact cctacgcttc cgttaacgat 1440
ctgggttttg agaataattt ttattgcccg gagcgtctga agctgaatct tgactggcag 1500
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gggatggcgc aggcgcggca ggttatcggg cagcttgagc atgaaagtag tcagcatgtg 1620
ccgtttgcta acgaaatggc tgagttgctg ttcgggcagt tggatgatgt gctgaatcgc 1680
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attaccggc tggcggctag cctgaaaagt ccctttgcgc tggataaatt ttgtgatgag 1800
gcatcgtgca gtgagcgcgt tttgcgtcag caatttcgcc agcagactgg aatgaccatc 1860
aatcaatatc tgcgacaggt cagagtgtgt catgcgcaat atcttctcca gcatagccgc 1920
ctgttaatat gtgatatttc gaccgaatgt ggctttgaag atagtaacta tttttcgggtg 1980
gtgtttacct gggaaaccgg gatgacgcc agccagtggc gtcactcaa ttcgcagaaa 2040
gattaa 2046

<210> 2
<211> 287
<212> DNA
<213> Escherichia coli

<220>
<221> promoter
<222> (1)..(287)
<223> rhaBAD promoter fragment containing rhaS and rhaR binding sites

<400> 2
actggcctcc tgatgtcgtc aacacggcga aatagtaatc acgaggtcag gttcttacct 60
taaattttcg acggaaaacc acgtaaaaaa cgtcgatttt tcaagataca gcgtgaattt 120

tcaggaaatg cggtgagcat cacatcacca caattcagca aattgtgaac atcatcacgt 180
tcattctttcc ctggttgcca atggcccatt ttctgtcag taacgagaag gtcgcgaatt 240
caggcgcttt ttagactggc cgtaatgaaa ttcagcagga tcacatt 287

<210> 3
<211> 125
<212> DNA
<213> Escherichia coli

<220>
<221> promoter
<222> (1)..(125)
<223> rhaBAD promoter fragment containing RhaS binding site

<400> 3
ttgtgaacat catcacgttc atctttccct ggttgccaat ggcccatttt cctgtcagta 60
acgagaaggt cgcgaattca ggcgcttttt agactggtcg taatgaaatt cagcaggatc 120
acatt 125

<210> 4
<211> 123
<212> DNA
<213> Escherichia coli

<220>
<221> promoter
<222> (1)..(123)
<223> rhaBAD promoter fragment containing RhaS binding site

<400> 4
atcaccacaa ttcagcaaatt tgtgaacatc atcacgttca tctttccctg gttgccaatg 60
ggcccattttc ctgtcagtaa cgagaaggtc gcgaattcag gcgcttttta gactggtcgt 120
aat 123

<210> 5
<211> 51
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)..(51)
<223> palindromic RhaS binding site of rhaBAD promoter

<400> 5
atctttccct ggttgccaat ggcccatttt cctgtcagta acgagaaggt c 51

<210> 6
<211> 1071
<212> DNA
<213> Alcaligenes faecalis

<220>

<221> CDS

<222> (1)..(1068)

<223> coding for nitrilase

<400> 6

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Met Gln Thr Arg Lys Ile Val Arg Ala Ala Val Gln Ala Ala Ser	
1 5 10 15	
ccc aac tac gat ctg gca acg ggt gtt gat aaa acc att gag ctg gct	96
Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala	
20 25 30	
cgt cag gcc cgc gat gag ggc tgt gac ctg atc gtg ttt ggt gaa acc	144
Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr	
35 40 45	
tgg ctg ccc gga tat ccc ttc cac gtc tgg ctg ggc gca ccg gcc tgg	192
Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp	
50 55 60	
tcg ctg aaa tac agt gcc cgc tac tat gcc aac tcg ctc tcg ctg gac	240
Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp	
65 70 75 80	
agt gca gag ttt caa cgc att gcc cag gcc gca cgg acc ttg ggt att	288
Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile	
85 90 95	
ttc atc gca ctg ggt tat agc gag cgc agc ggc ggc agc ctt tac ctg	336
Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu	
100 105 110	
ggc caa tgc ctg atc gac gac aag ggc gag atg ctg tgg tcg cgt cgc	384
Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg	
115 120 125	
aaa ctc aaa ccc acg cat gta gag cgc acc gta ttt ggt gaa ggt tat	432
Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr	
130 135 140	
gcc cgt gat ctg att gtg tcc gac aca gaa ctg gga cgc gtc ggt gct	480
Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala	
145 150 155 160	
cta tgc tgc tgg gag cat ttg tcg ccc ttg agc aag tac gcg ctg tac	528
Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr	
165 170 175	
tcc cag cat gaa gcc att cac att gct gcc tgg ccg tcg ttt tcg cta	576
Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu	
180 185 190	
tac agc gaa cag gcc cac gcc ctc agt gcc aag gtg aac atg gct gcc	624
Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala	
195 200 205	
tcg caa atc tat tcg gtt gaa ggc cag tgc ttt acc atc gcc gcc agc	672
Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser	
210 215 220	
agt gtg gtc acc caa gag acg cta gac atg ctg gaa gtg ggt gaa cac	720
Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu His	
225 230 235 240	
aac gcc ccc ttg ctg aaa gtg ggc ggc ggc agt tcc atg att ttt gcg	768
Asn Ala Pro Leu Leu Lys Val Gly Gly Gly Ser Ser Met Ile Phe Ala	
245 250 255	
ccg gac gga cgc aca ctg gct ccc tac ctg cct cac gat gcc gag ggc	816
Pro Asp Gly Arg Thr Leu Ala Pro Tyr Leu Pro His Asp Ala Glu Gly	
260 265 270	
ttg atc att gcc gat ctg aat atg gag gag att gcc ttc gcc aaa gcg	864

Leu Ile Ile Ala Asp Leu Asn Met Glu Glu Ile Ala Phe Ala Lys Ala	
275 280 285	
atc aat gac ccc gta ggc cac tat tcc aaa ccc gag gcc acc cgt ctg	912
Ile Asn Asp Pro Val Gly His Tyr Ser Lys Pro Glu Ala Thr Arg Leu	
290 295 300	
gtg ctg gac ttg ggg cac cga gac ccc atg act cgg gtg cac tcc aaa	960
Val Leu Asp Leu Gly His Arg Asp Pro Met Thr Arg Val His Ser Lys	
305 310 315 320	
agc gtg acc agg gaa gag gct ccc gag caa ggt gtg caa agc aag att	1008
Ser Val Thr Arg Glu Glu Ala Pro Glu Gln Gly Val Gln Ser Lys Ile	
325 330 335	
gcc tca gtc gct atc agc cat cca cag gac tcg gac aca ctg cta gtg	1056
Ala Ser Val Ala Ile Ser His Pro Gln Asp Ser Asp Thr Leu Leu Val	
340 345 350	
caa gag ccg tct tga	1071
Gln Glu Pro Ser	
355	

<210> 7

<211> 356

<212> PRT

<213> *Alcaligenes faecalis*

<400> 7

Met Gln Thr Arg Lys Ile Val Arg Ala Ala Ala Val Gln Ala Ala Ser	
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20 25 30	
Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr	
35 40 45	
Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp	
50 55 60	
Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp	
65 70 75 80	
Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile	
85 90 95	
Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu	
100 105 110	
Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg	
115 120 125	
Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr	
130 135 140	
Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala	
145 150 155 160	
Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr	
165 170 175	
Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu	
180 185 190	
Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala	
195 200 205	
Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser	
210 215 220	
Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu His	
225 230 235 240	
Asn Ala Pro Leu Leu Lys Val Gly Gly Gly Ser Ser Met Ile Phe Ala	
245 250 255	

[illegible]

cac tgc aaa gcc agc cgt cgc gtt tcg gcc tat ttt ggc gag caa ctc	528
His Cys Lys Ala Ser Arg Arg Val Ser Ala Tyr Phe Gly Glu Gln Leu	
165 170 175	
ggc aca cca tcg gtg atg aac atc tgg atc ccg gat ggt atg aaa gat	576
Gly Thr Pro Ser Val Met Asn Ile Trp Ile Pro Asp Gly Met Lys Asp	
180 185 190	
atc acc gtt gac cgt ctc gcc ccg cgt cag cgt ctg ctg gca gca ctg	624
Ile Thr Val Asp Arg Leu Ala Pro Arg Gln Arg Leu Leu Ala Ala Leu	
195 200 205	
gat gag gtg atc agc gag aag cta aac cct gcg cac cat atc gac gcc	672
Asp Glu Val Ile Ser Glu Lys Leu Asn Pro Ala His His Ile Asp Ala	
210 215 220	
gtt gag agc aaa ttg ttt ggc att ggc gca gag agc tac acg gtt ggc	720
Val Glu Ser Lys Leu Phe Gly Ile Gly Ala Glu Ser Tyr Thr Val Gly	
225 230 235 240	
tcc aat gag ttt tac atg ggg tat gcc acc agc cgc cag act gcg ctg	768
Ser Asn Glu Phe Tyr Met Gly Tyr Ala Thr Ser Arg Gln Thr Ala Leu	
245 250 255	
tgc ctg gac gcc ggg cac ttc cac ccg act gaa gtg att tcc gac aag	816
Cys Leu Asp Ala Gly His Phe His Pro Thr Glu Val Ile Ser Asp Lys	
260 265 270	
att tcc gcc gcc atg ctg tat gtg ccg cag ttg ctg ctg cac gtc agc	864
Ile Ser Ala Ala Met Leu Tyr Val Pro Gln Leu Leu Leu His Val Ser	
275 280 285	
cgt ccg gtt cgc tgg gac agc gat cac gta gtg ctg ctg gat gat gaa	912
Arg Pro Val Arg Trp Asp Ser Asp His Val Val Leu Leu Asp Asp Glu	
290 295 300	
acc cag gca att gcc agt gag att gtg cgt cac gat ctg ttt gac cgg	960
Thr Gln Ala Ile Ala Ser Glu Ile Val Arg His Asp Leu Phe Asp Arg	
305 310 315 320	
gtg cat atc ggc ctt gac ttc ttc gat gcc tct atc aac cgc att gcc	1008
Val His Ile Gly Leu Asp Phe Phe Asp Ala Ser Ile Asn Arg Ile Ala	
325 330 335	
gcg tgg gtc att ggt aca cgc aat atg aaa aaa gcc ctg ctg cgt gcg	1056
Ala Trp Val Ile Gly Thr Arg Asn Met Lys Lys Ala Leu Leu Arg Ala	
340	